

SEQUENCE LISTING

<110> AVENTIS PHARMA SA  
THE GOVERNMENT OF THE UNITED STATES,

<120> NUCLEIC ACIDS OF THE HUMAN ABCC12 GENE, VECTORS  
CONTAINING SUCH NUCLEIC ACIDS, AND USES THEREOF

<130> ABCC12 GENE

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<141> 2002-03-05

<150> 60/272,759

<151> 2001-03-05

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<170> PatentIn Ver. 2.1

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gttcacccac atcacctcct ccatgcaggg cctgggcac atcacgcct atggcaagaa 120  
ggagagctgc atcaccta 138

<210> 24  
<211> 157  
<212> DNA  
<213> Homo sapiens

<400> 24  
tcacctctc tactttaact gtgctctcag gtggtttgcg ctgagaatgg atgtcctcat 60  
gaacatcctt accttcactg tggccttggt ggtgaccctg agtttctcct ccatcagtac 120  
ttcatccaaa ggctgtcat tgctatacat catccag 157

<210> 25  
<211> 90  
<212> DNA  
<213> Homo sapiens

<400> 25  
ctgagcggac tgctccaagt gtgtgtgcga acgggaacag agacgcaagc caaattcacc 60

tccgtggagc tgctcagga atacatttcg

90

<210> 26  
<211> 190  
<212> DNA  
<213> Homo sapiens

<400> 26  
acctgtgttc ctgaatgcac tcatccctc aaagtgggga cctgtcccaa ggactggccc 60  
agctgtgggg agatcacctt cagagactat cagatgagat acagagacaa cccccctt 120  
gttctcgaca gcctgaactt gaacatacaa agtgggcaga cagtcgggat tggtggaaga 180  
acaggttccg 190

<210> 27  
<211> 160  
<212> DNA  
<213> Homo sapiens

<400> 27  
gaaagtcac gtttaggaatg gctttgtttc gtctggtgga gccagccagt ggcacaatct 60  
ttattgatga ggtggatata tgcattctca gcttgggaaga cctcagaacc aagctgactg 120  
tgatcccaca ggatcctgtc ctgtttgtag gtacagtaag 160

<210> 28  
<211> 79  
<212> DNA  
<213> Homo sapiens

<400> 28  
gtacaacttg gatccctttg agagtcacac cgatgagatg ctctggcagg ttctggagag 60  
aacattcatg agagacaca 79

<210> 29  
<211> 114  
<212> DNA  
<213> Homo sapiens

<400> 29  
ataatgaaac tcccagaaaa attacaggca gaagtcacag aaaatggaga aaactttctca 60  
gtagggggaac gtcagctgct ttgtgtggcc cgagctcttc tccgtaattc aaag 114

<210> 30  
<211> 165  
<212> DNA  
<213> Homo sapiens

<400> 30  
atcattctcc ttgatgaagc caccgctct atggactcca agactgacac cctgggttcag 60  
aacaccatca aagatgcctt caagggctgc actgtgctga ccacgcccc ccgctcaac 120  
acagttctca actgcgatca cgtcctgggt atggaaaatg ggaag 165

<210> 31  
<211> 289  
<212> DNA  
<213> Homo sapiens



<400> 31  
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 ttactagcag cagaagtcag attgtagagg tcctggcggc tgattctaga ggaggaagag 120  
 gctctgtgag atgaatagga ggagtcctca ggaggagggg ctgtcctctc cgcaggcagc 180  
 cctggctctc agccctccc atccacggag tgagctgggg ctgaagttgt cccactgcc 240  
 atactcagtc catgtcaccc cacttggtgg gcttgggggtt ggttctggg 289

<210> 32  
 <211> 85  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
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 agagaggaag atgctggtat aatcg 85

<210> 33  
 <211> 1356  
 <212> PRT  
 <213> Homo sapiens

<400> 33  
 Met Val Gly Glu Gly Pro Tyr Leu Ile Ser Asp Leu Asp Gln Arg Gly  
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 Arg Arg Arg Ser Phe Ala Glu Arg Tyr Asp Pro Ser Leu Lys Thr Met  
 20 25 30  
 Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp  
 35 40 45  
 Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met  
 50 55 60  
 Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu  
 65 70 75 80  
 Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu  
 85 90 95  
 Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser  
 100 105 110  
 His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val  
 115 120 125  
 Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu  
 130 135 140  
 Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp  
 145 150 155 160  
 Val Gly Ile Gly Leu Cys Ile Ala Leu Phe Ala Thr Glu Phe Thr Lys  
 165 170 175  
 Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile  
 180 185 190





Gln Trp Val Tyr Thr Ala Ser Met Val Phe Met Leu Val Phe Gly Val  
 850 855 860  
 Thr Lys Gly Phe Val Phe Thr Lys Thr Thr Leu Met Ala Ser Ser Ser  
 865 870 875 880  
 Leu His Asp Thr Val Phe Asp Lys Ile Leu Lys Ser Pro Met Ser Phe  
 885 890 895  
 Phe Asp Thr Thr Pro Thr Gly Arg Leu Met Asn Arg Phe Ser Lys Asp  
 900 905 910  
 Met Asp Glu Leu Asp Val Arg Leu Pro Phe His Ala Glu Asn Phe Leu  
 915 920 925  
 Gln Gln Phe Phe Met Val Val Phe Ile Leu Val Ile Leu Ala Ala Val  
 930 935 940  
 Phe Pro Ala Val Leu Leu Val Val Ala Ser Leu Ala Val Gly Phe Phe  
 945 950 955 960  
 Ile Leu Leu Arg Ile Phe His Arg Gly Val Gln Glu Leu Lys Lys Val  
 965 970 975  
 Glu Asn Val Ser Arg Ser Pro Trp Phe Thr His Ile Thr Ser Ser Met  
 980 985 990  
 Gln Gly Leu Gly Ile Ile His Ala Tyr Gly Lys Lys Glu Ser Cys Ile  
 995 1000 1005  
 Thr Tyr His Leu Leu Tyr Phe Asn Cys Ala Leu Arg Trp Phe Ala Leu  
 1010 1015 1020  
 Arg Met Asp Val Leu Met Asn Ile Leu Thr Phe Thr Val Ala Leu Leu  
 1025 1030 1035 1040  
 Val Thr Leu Ser Phe Ser Ser Ile Ser Thr Ser Ser Lys Gly Leu Ser  
 1045 1050 1055  
 Leu Ser Tyr Ile Ile Gln Leu Ser Gly Leu Leu Gln Val Cys Val Arg  
 1060 1065 1070  
 Thr Gly Thr Glu Thr Gln Ala Lys Phe Thr Ser Val Glu Leu Leu Arg  
 1075 1080 1085  
 Glu Tyr Ile Ser Thr Cys Val Pro Glu Cys Thr His Pro Leu Lys Val  
 1090 1095 1100  
 Gly Thr Cys Pro Lys Asp Trp Pro Ser Cys Gly Glu Ile Thr Phe Arg  
 1105 1110 1115 1120  
 Asp Tyr Gln Met Arg Tyr Arg Asp Asn Thr Pro Leu Val Leu Asp Ser  
 1125 1130 1135  
 Leu Asn Leu Asn Ile Gln Ser Gly Gln Thr Val Gly Ile Val Gly Arg  
 1140 1145 1150  
 Thr Gly Ser Gly Lys Ser Ser Leu Gly Met Ala Leu Phe Arg Leu Val  
 1155 1160 1165

Glu Pro Ala Ser Gly Thr Ile Phe Ile Asp Glu Val Asp Ile Cys Ile  
 1170 1175 1180  
 Leu Ser Leu Glu Asp Leu Arg Thr Lys Leu Thr Val Ile Pro Gln Asp  
 1185 1190 1195 1200  
 Pro Val Leu Phe Val Gly Thr Val Arg Tyr Asn Leu Asp Pro Phe Glu  
 1205 1210 1215  
 Ser His Thr Asp Glu Met Leu Trp Gln Val Leu Glu Arg Thr Phe Met  
 1220 1225 1230  
 Arg Asp Thr Ile Met Lys Leu Pro Glu Lys Leu Gln Ala Glu Val Thr  
 1235 1240 1245  
 Glu Asn Gly Glu Asn Phe Ser Val Gly Glu Arg Gln Leu Leu Cys Val  
 1250 1255 1260  
 Ala Arg Ala Leu Leu Arg Asn Ser Lys Ile Ile Leu Leu Asp Glu Ala  
 1265 1270 1275 1280  
 Thr Ala Ser Met Asp Ser Lys Thr Asp Thr Leu Val Gln Asn Thr Ile  
 1285 1290 1295  
 Lys Asp Ala Phe Lys Gly Cys Thr Val Leu Thr Ile Ala His Arg Leu  
 1300 1305 1310  
 Asn Thr Val Leu Asn Cys Asp His Val Leu Val Met Glu Asn Gly Lys  
 1315 1320 1325  
 Val Ile Glu Phe Asp Lys Pro Glu Val Leu Ala Glu Lys Pro Asp Ser  
 1330 1335 1340  
 Ala Phe Ala Met Leu Leu Ala Ala Glu Val Arg Leu  
 1345 1350 1355

<210> 34  
 <211> 1359  
 <212> PRT  
 <213> Homo sapiens

<400> 34  
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 Arg Arg Arg Ser Phe Ala Glu Arg Tyr Asp Pro Ser Leu Lys Thr Met  
 20 25 30  
 Ile Pro Val Arg Pro Cys Ala Arg Leu Ala Pro Asn Pro Val Asp Asp  
 35 40 45  
 Ala Gly Leu Leu Ser Phe Ala Thr Phe Ser Trp Leu Thr Pro Val Met  
 50 55 60  
 Val Lys Gly Tyr Arg Gln Arg Leu Thr Val Asp Thr Leu Pro Pro Leu  
 65 70 75 80  
 Ser Thr Tyr Asp Ser Ser Asp Thr Asn Ala Lys Arg Phe Arg Val Leu  
 85 90 95

Trp Asp Glu Glu Val Ala Arg Val Gly Pro Glu Lys Ala Ser Leu Ser  
100 105 110

His Val Val Trp Lys Phe Gln Arg Thr Arg Val Leu Met Asp Ile Val  
115 120 125

Ala Asn Ile Leu Cys Ile Ile Met Ala Ala Ile Gly Pro Thr Val Leu  
130 135 140

Ile His Gln Ile Leu Gln Gln Thr Glu Arg Thr Ser Gly Lys Val Trp  
145 150 155 160

Val Gly Ile Gly Leu Cys Ile Ala Leu Phe Ala Thr Glu Phe Thr Lys  
165 170 175

Val Phe Phe Trp Ala Leu Ala Trp Ala Ile Asn Tyr Arg Thr Ala Ile  
180 185 190

Arg Leu Lys Val Ala Leu Ser Thr Leu Val Phe Glu Asn Leu Val Ser  
195 200 205

Phe Lys Thr Leu Thr His Ile Ser Val Gly Glu Val Leu Asn Ile Leu  
210 215 220

Ser Ser Asp Ser Tyr Ser Leu Phe Glu Ala Ala Leu Phe Cys Pro Leu  
225 230 235 240

Pro Ala Thr Ile Pro Ile Leu Met Val Phe Cys Ala Ala Tyr Ala Phe  
245 250 255

Phe Ile Leu Gly Pro Thr Ala Leu Ile Gly Ile Ser Val Tyr Val Ile  
260 265 270

Phe Ile Pro Val Gln Met Phe Met Ala Lys Leu Asn Ser Ala Phe Arg  
275 280 285

Arg Ser Ala Ile Leu Val Thr Asp Lys Arg Val Gln Thr Met Asn Glu  
290 295 300

Phe Leu Thr Cys Ile Arg Leu Ile Lys Met Tyr Ala Trp Glu Lys Ser  
305 310 315 320

Phe Thr Asn Thr Ile Gln Asp Ile Arg Arg Arg Glu Arg Lys Leu Leu  
325 330 335

Glu Lys Ala Gly Phe Val Gln Ser Gly Asn Ser Ala Leu Ala Pro Ile  
340 345 350

Val Ser Thr Ile Ala Ile Val Leu Thr Leu Ser Cys His Ile Leu Leu  
355 360 365

Arg Arg Lys Leu Thr Ala Pro Val Ala Phe Ser Val Ile Ala Met Phe  
370 375 380

Asn Val Met Lys Phe Ser Ile Ala Ile Leu Pro Phe Ser Ile Lys Ala  
385 390 395 400

Met Ala Glu Ala Asn Val Ser Leu Arg Arg Met Lys Lys Ile Leu Ile  
405 410 415

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Asp Lys Ser Pro Pro Ser Tyr Ile Thr Gln Pro Glu Asp Pro Asp Thr
      420                      425                      430

Val Leu Leu Leu Ala Asn Ala Thr Leu Thr Trp Glu His Glu Ala Ser
      435                      440                      445

Arg Lys Ser Thr Pro Lys Lys Leu Gln Asn Gln Lys Arg His Leu Cys
      450                      455                      460

Lys Lys Gln Arg Ser Glu Ala Tyr Ser Glu Arg Ser Pro Pro Ala Lys
      465                      470                      475                      480

Gly Ala Thr Gly Pro Glu Glu Gln Ser Asp Ser Leu Lys Ser Val Leu
      485                      490                      495

His Ser Ile Ser Phe Val Val Arg Lys Gly Lys Ile Leu Gly Ile Cys
      500                      505                      510

Gly Asn Val Gly Ser Gly Lys Ser Ser Leu Leu Ala Ala Leu Leu Gly
      515                      520                      525

Gln Met Gln Leu Gln Lys Gly Val Val Ala Val Asn Gly Thr Leu Ala
      530                      535                      540

Tyr Val Ser Gln Gln Ala Trp Ile Phe His Gly Asn Val Arg Glu Asn
      545                      550                      555                      560

Ile Leu Phe Gly Glu Lys Tyr Asp His Gln Arg Tyr Gln His Thr Val
      565                      570                      575

Arg Val Cys Gly Leu Gln Lys Asp Leu Ser Asn Leu Pro Tyr Gly Asp
      580                      585                      590

Leu Thr Glu Ile Gly Glu Arg Gly Leu Asn Leu Ser Gly Gly Gln Arg
      595                      600                      605

Gln Arg Ile Ser Leu Ala Arg Ala Val Tyr Ser Asp Arg Gln Leu Tyr
      610                      615                      620

Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala His Val Gly Lys His
      625                      630                      635                      640

Val Phe Glu Glu Cys Ile Lys Lys Thr Leu Arg Gly Lys Thr Val Val
      645                      650                      655

Leu Val Thr His Gln Leu Gln Phe Leu Glu Ser Cys Asp Glu Val Ile
      660                      665                      670

Leu Leu Glu Asp Gly Glu Ile Cys Glu Lys Gly Thr His Lys Glu Leu
      675                      680                      685

Met Glu Glu Arg Gly Arg Tyr Ala Lys Leu Ile His Asn Leu Arg Gly
      690                      695                      700

Leu Gln Phe Lys Asp Pro Glu His Leu Tyr Asn Ala Ala Met Val Glu
      705                      710                      715                      720

Ala Phe Lys Glu Ser Pro Ala Glu Arg Glu Glu Asp Ala Gly Ile Ile
      725                      730                      735

Val Leu Ala Pro Gly Asn Glu Lys Asp Glu Gly Lys Glu Ser Glu Thr

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740					745					750					
Gly	Ser	Glu	Phe	Val	Asp	Thr	Lys	Val	Pro	Glu	His	Gln	Leu	Ile	Gln
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Thr	Glu	Ser	Pro	Gln	Glu	Gly	Thr	Val	Thr	Trp	Lys	Thr	Tyr	His	Thr
	770					775					780				
Tyr	Ile	Lys	Ala	Ser	Gly	Gly	Tyr	Leu	Leu	Ser	Leu	Phe	Thr	Val	Phe
785					790					795					800
Leu	Phe	Leu	Leu	Met	Ile	Gly	Ser	Ala	Ala	Phe	Ser	Asn	Trp	Trp	Leu
				805					810					815	
Gly	Leu	Trp	Leu	Asp	Lys	Gly	Ser	Arg	Met	Thr	Cys	Gly	Pro	Gln	Gly
			820					825					830		
Asn	Arg	Thr	Met	Cys	Glu	Val	Gly	Ala	Val	Leu	Ala	Asp	Ile	Gly	Gln
		835					840					845			
His	Val	Tyr	Gln	Trp	Val	Tyr	Thr	Ala	Ser	Met	Val	Phe	Met	Leu	Val
	850					855					860				
Phe	Gly	Val	Thr	Lys	Gly	Phe	Val	Phe	Thr	Lys	Thr	Thr	Leu	Met	Ala
865					870					875					880
Ser	Ser	Ser	Leu	His	Asp	Thr	Val	Phe	Asp	Lys	Ile	Leu	Lys	Ser	Pro
				885					890					895	
Met	Ser	Phe	Phe	Asp	Thr	Thr	Pro	Thr	Gly	Arg	Leu	Met	Asn	Arg	Phe
			900					905					910		
Ser	Lys	Asp	Met	Asp	Glu	Leu	Asp	Val	Arg	Leu	Pro	Phe	His	Ala	Glu
		915					920					925			
Asn	Phe	Leu	Gln	Gln	Phe	Phe	Met	Val	Val	Phe	Ile	Leu	Val	Ile	Leu
	930					935					940				
Ala	Ala	Val	Phe	Pro	Ala	Val	Leu	Leu	Val	Val	Ala	Ser	Leu	Ala	Val
945					950					955					960
Gly	Phe	Phe	Ile	Leu	Leu	Arg	Ile	Phe	His	Arg	Gly	Val	Gln	Glu	Leu
				965					970					975	
Lys	Lys	Val	Glu	Asn	Val	Ser	Arg	Ser	Pro	Trp	Phe	Thr	His	Ile	Thr
			980					985					990		
Ser	Ser	Met	Gln	Gly	Leu	Gly	Ile	Ile	His	Ala	Tyr	Gly	Lys	Lys	Glu
		995					1000					1005			
Ser	Cys	Ile	Thr	Tyr	His	Leu	Leu	Tyr	Phe	Asn	Cys	Ala	Leu	Arg	Trp
	1010					1015					1020				
Phe	Ala	Leu	Arg	Met	Asp	Val	Leu	Met	Asn	Ile	Leu	Thr	Phe	Thr	Val
1025					1030					1035					1040
Ala	Leu	Leu	Val	Thr	Leu	Ser	Phe	Ser	Ser	Ile	Ser	Thr	Ser	Ser	Lys
				1045					1050					1055	
Gly	Leu	Ser	Leu	Ser	Tyr	Ile	Ile	Gln	Leu	Ser	Gly	Leu	Leu	Gln	Val
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<210> 35
<211> 18
<212> DNA
<213> Artificial Sequence
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<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 35

tccttcgccca cattttcc

18

<210> 36

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 36

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18

<210> 37

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 37

ttctcattca ccaaattcctc c

21

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 38

acattaaaca tggcaatcac ac

22

<210> 39

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 39

gtgtgattgc catgtttaat gt

22

<210> 40

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of the Artificial Sequence: PRIMER

<400> 40

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20

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 41

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18

<210> 42

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 42

cactgcaagc atggtgttc

19

<210> 43

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 43

ctcatcggtg tgactctca

19

<210> 44

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 44

tttgagagtc acaccgatga gat

23

<210> 45

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 45

cccagaacca accccaag

18

<210> 46

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the Artificial Sequence: PRIMER

<400> 46

ggctctgtga gatgaatagg

20